

51791AUSC1.ST25.txt  
SEQUENCE LISTING

<110> Harkins, Richard  
Parkes, Deborah  
Parry, Gordon  
Schneider, Douglas  
Steinbrecher, Renate

<120> DNA Encoding a Novel RG-1 Polypeptide

<130> 51791AUSC1

<150> US 60/172,370  
<151> 1999-12-16

<150> US 09/732,357  
<151> 2000-12-07

<160> 31

<170> PatentIn version 3.1

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Met  
1  
gaa aac ccc agc ccg gcc gcc ctg ggc aag gcc ctc tgc gct ctc 346  
Glu Asn Pro Ser Pro Ala Ala Ala Leu Gly Lys Ala Leu Cys Ala Leu  
5 10 15  
ctc ctg gcc act ctc ggc gcc ggc cag cct ctt ggg gga gag tcc 394  
Leu Leu Ala Thr Leu Gly Ala Ala Gly Gln Pro Leu Gly Gly Glu Ser  
20 25 30  
atc tgt tcc gcc gga gcc ccg gcc aaa tac agc atc acc ttc acg ggc 442  
Ile Cys Ser Ala Gly Ala Pro Ala Lys Tyr Ser Ile Thr Phe Thr Gly  
35 40 45  
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## 51791AUSC1.ST25.txt

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Pro	Ala	Gln	Trp	Ser	Ser	Leu	Leu	Gly	Ala	Ala	His	Ser	Ser	Asp	Tyr	
						70			75			80				
agc atg tgg agg aag aac cag tac gtc agt aac ggg ctg cgc gac ttt															586	
Ser	Met	Trp	Arg	Lys	Asn	Gln	Tyr	Val	Ser	Asn	Gly	Leu	Arg	Asp	Phe	
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gcf gag cgc ggc gag gcc tgg gcf ctg atg aag gag atc gag gcf gcf															634	
Ala	Glu	Arg	Gly	Glu	Ala	Trp	Ala	Leu	Met	Lys	Glu	Ile	Glu	Ala	Ala	
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ggg gag gcf ctg cag acg gtg cac gcf gtg ttt tcg gcf ccc gcc gtc															682	
Gly	Glu	Ala	Leu	Gln	Ser	Val	His	Ala	Val	Phe	Ser	Ala	Pro	Ala	Val	
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ccc acg ggc acc ggg cag acg tcg gcf gag ctg gag gtg cag cgc agg															730	
Pro	Ser	Gly	Thr	Gly	Gln	Thr	Ser	Ala	Glu	Leu	Glu	Val	Gln	Arg	Arg	
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cac tcg ctg gtc tcg ttt gtg gtg cgc atc gtg ccc acg ccc gac tgg															778	
His	Ser	Leu	Val	Ser	Phe	Val	Val	Arg	Ile	Val	Pro	Ser	Pro	Asp	Trp	
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ttc gtg ggc gtg gac acg ctg gac ctg tgc gac ggg gac cgt tgg cgg															826	
Phe	Val	Gly	Val	Asp	Ser	Leu	Asp	Leu	Cys	Asp	Gly	Asp	Arg	Trp	Arg	
					165			170			175					
gaa cag gcf gcf ctg gac ctg tac ccc tac gac gcc ggg acg gac acg															874	
Glu	Gln	Ala	Ala	Leu	Asp	Leu	Tyr	Pro	Tyr	Asp	Ala	Gly	Thr	Asp	Ser	
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ggc ttc acc ttc tcc ccc aac ttc gcc acc atc ccg cag gac acg															922	
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Val	Thr	Glu	Ile	Thr	Ser	Ser	Pro	Ser	His	Pro	Ala	Asn	Ser	Phe		
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tac tac cca cgg ctg aag gcc ctg cct ccc atc gcc agg gtg aca ctg															1018	
Tyr	Tyr	Pro	Arg	Leu	Lys	Ala	Leu	Pro	Pro	Ile	Ala	Arg	Val	Thr	Leu	
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Val	Arg	Leu	Arg	Gln	Ser	Pro	Arg	Ala	Phe	Ile	Pro	Pro	Ala	Pro	Val	
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ctg ccc acg agg gac aat gag att gta gac acg gcc tca gtt cca gaa															1114	
Leu	Pro	Ser	Arg	Asp	Asn	Glu	Ile	Val	Asp	Ser	Ala	Ser	Val	Pro	Glu	
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acg ccg ctg gac tgc gag gtc tcc ctg tgg tcg tcc tgg gga ctg tgc															1162	
Thr	Pro	Leu	Asp	Cys	Glu	Val	Ser	Leu	Trp	Ser	Ser	Trp	Gly	Leu	Cys	
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## 51791AUSC1.ST25.txt

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gag gct gag tgc gtc cct gat aac tgc gtc taa gaccagagcc ccgcagcccc Glu Ala Glu Cys Val Pro Asp Asn Cys Val 325 330	1311
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Ser Ile Cys Ser Ala Gly Ala Pro Ala Lys Tyr Ser Ile Thr Phe Thr 35 40 45
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Gly Lys Trp Ser Gln Thr Ala Phe Pro Lys Gln Tyr Pro Leu Phe Arg 50 55 60
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Pro Pro Ala Gln Trp Ser Ser Leu Leu Gly Ala Ala His Ser Ser Asp 65 70 75 80
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Tyr Ser Met Trp Arg Lys Asn Gln Tyr Val Ser Asn Gly Leu Arg Asp 85 90 95
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51791AUSC1.ST25.txt

Phe Ala Glu Arg Gly Glu Ala Trp Ala Leu Met Lys Glu Ile Glu Ala  
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Ala Gly Glu Ala Leu Gln Ser Val His Ala Val Phe Ser Ala Pro Ala  
115 120 125

Val Pro Ser Gly Thr Gly Gln Thr Ser Ala Glu Leu Glu Val Gln Arg  
130 135 140

Arg His Ser Leu Val Ser Phe Val Val Arg Ile Val Pro Ser Pro Asp  
145 150 155 160

Trp Phe Val Gly Val Asp Ser Leu Asp Leu Cys Asp Gly Asp Arg Trp  
165 170 175

Arg Glu Gln Ala Ala Leu Asp Leu Tyr Pro Tyr Asp Ala Gly Thr Asp  
180 185 190

Ser Gly Phe Thr Phe Ser Ser Pro Asn Phe Ala Thr Ile Pro Gln Asp  
195 200 205

Thr Val Thr Glu Ile Thr Ser Ser Ser Pro Ser His Pro Ala Asn Ser  
210 215 220

Phe Tyr Tyr Pro Arg Leu Lys Ala Leu Pro Pro Ile Ala Arg Val Thr  
225 230 235 240

Leu Val Arg Leu Arg Gln Ser Pro Arg Ala Phe Ile Pro Pro Ala Pro  
245 250 255

Val Leu Pro Ser Arg Asp Asn Glu Ile Val Asp Ser Ala Ser Val Pro  
260 265 270

Glu Thr Pro Leu Asp Cys Glu Val Ser Leu Trp Ser Ser Trp Gly Leu  
275 280 285

Cys Gly Gly His Cys Gly Arg Leu Gly Thr Lys Ser Arg Thr Arg Tyr  
290 295 300

Val Arg Val Gln Pro Ala Asn Asn Gly Ser Pro Cys Pro Glu Leu Glu  
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Glu Glu Ala Glu Cys Val Pro Asp Asn Cys Val  
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Leu Phe Arg

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Thr Ile Pro Gln Asp Thr Val  
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Val Cys Thr Ala Arg Pro Leu Ala Arg Tyr Ser Ile Thr Phe Thr Gly  
35 40 45

Lys Trp Ser Gln Thr Ala Phe Pro Lys Gln Tyr Pro Leu Phe Arg Pro  
50 55 60

Pro Ala Gln Trp Ser Ser Leu Leu Gly Ala Ala His Ser Ser Asp Tyr  
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Ser Met Trp Arg Lys Asn Glu Tyr Val Ser Asn Gly Leu Arg Asp Phe  
85 90 95

Ala Glu Arg Gly Glu Ala Trp Ala Leu Met Lys Glu Ile Glu Ala Ala  
100 105 110

Gly Glu Lys Leu Gln Ser Val His Ala Val Phe Ser Ala Pro Ala Val  
115 120 125

Pro Ser Gly Thr Gly Gln Thr Ser Ala Glu Leu Glu Val His Pro Arg  
130 135 140

His Ser Leu Val Ser Phe Val Val Arg Ile Val Pro Ser Pro Asp Trp  
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Phe Val Gly Ile Asp Ser Leu Asp Leu Cys Glu Gly Gly Arg Trp Lys

## 51791AUSC1.ST25.txt

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Gly Phe Thr Phe Ser Ser Pro Asn Phe Ala Thr Ile Pro Gln Asp Thr  
 195 200 205

Val Thr Glu Ile Thr Ala Ser Ser Pro Ser His Pro Ala Asn Ser Phe  
 210 215 220

Tyr Tyr Pro Arg Leu Lys Ser Leu Pro Pro Ile Ala Lys Val Thr Phe  
 225 230 235 240

Val Arg Leu Arg Gln Ser Pro Arg Ala Phe Ala Pro Pro Ser Leu Asp  
 245 250 255

Leu Ala Ser Arg Gly Asn Glu Ile Val Asp Ser Leu Ser Val Pro Glu  
 260 265 270

Thr Pro Leu Asp Cys Glu Val Ser Leu Trp Ser Ser Trp Gly Leu Cys  
 275 280 285

Gly Gly Pro Cys Gly Lys Leu Gly Ala Lys Ser Arg Thr Arg Tyr Val  
 290 295 300

Arg Val Gln Pro Ala Asn Asn Gly Thr Pro Cys Pro Glu Leu Glu Glu  
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Glu Ala Glu Cys Ala Pro Asp Asn Cys Val  
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&lt;212&gt; DNA

&lt;213&gt; artificial sequence

&lt;220&gt;

&lt;223&gt; primer

&lt;400&gt; 14

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&lt;210&gt; 15

&lt;211&gt; 45

&lt;212&gt; DNA

&lt;213&gt; artificial sequence

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ctctcctgca gggccagtca gagtggtagc agcagctact tagcctggta ccagcagaaa	180
cctggccagg ctccccaggct cctcatctat ggtgcaccca gcagggccac tggcatccca	240
gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag	300
cctgaagatt ttgcagtgtta ttactgtcag cagtatagtta gctcgctcac tttcggcggg	360
gggaccaagg tggagatcaa a	381

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&lt;211&gt; 441

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 21

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gttcagctgg tgcagtctgg gggaggctt g t acatcctg gggggccct gagactctcc	120
tgtgcaggct ctggattcac cttagtgc tatgttatgc actggcttcg ccaggctcca	180
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gtctcttcag cttccaccaa g	441

&lt;210&gt; 22

&lt;211&gt; 441

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 22

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tccgtgaagg gccgattcac catctccaga gacaatgccaa agaactcctt gtatcttcaa	300
atgaacagcc tgagagccga ggacacggct gtgtattact gtgcaagatg gggttactat	360

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cctggccagg ctcccaggct cctcatctat ggtgcacatcca gcagggccac tggcatccca	240
gacagggtca gtggcagtgg gtctggaca gacttcactc tcaccatcag cagactggag	300
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tccgtgaagg gccgattcac catctccaga gacaatgcca agaactcctt gtatcttcaa	300
atgaacagcc tgagagccga ggacatggct gtgtattact gtcaagatg gggggactgg	360
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atgaacagcc	tgagagccga	ggacacggct	gtgtattact	gtgcaagatg	gggggactgg	360
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<400> 26

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					20			25					30		

Leu	Ser	Pro	Gly	Glu	Arg	Ala	Thr	Leu	Ser	Cys	Arg	Ala	Ser	Gln	Ser
					35			40			45				

Val	Ser	Ser	Ser	Tyr	Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ala
					50			55			60				

Pro	Arg	Leu	Leu	Ile	Tyr	Gly	Ala	Ser	Ser	Arg	Ala	Thr	Gly	Ile	Pro
					65			70			75			80	

Asp	Arg	Phe	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile		
					85			90			95				

Ser	Arg	Leu	Glu	Pro	Glu	Asp	Phe	Ala	Val	Tyr	Tyr	Cys	Gln	Gln	Tyr
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Ser	Ser	Ser	Leu	Thr	Phe	Gly	Gly	Thr	Lys	Val	Glu	Ile	Lys		
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51791AUSC1.ST25.txt

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20 25 30

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe  
35 40 45

Ser Ser Tyr Val Met His Trp Leu Arg Gln Ala Pro Gly Lys Gly Leu  
50 55 60

Glu Trp Val Ser Val Ile Gly Thr Gly Gly Val Thr His Tyr Ala Asp  
65 70 75 80

Ser Val Lys Gly Arg Phe Met Ile Ser Arg Asp Asn Ala Lys Asn Ser  
85 90 95

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Met Tyr  
100 105 110

Tyr Cys Ala Arg Trp Gly Tyr Tyr Gly Ser Gly Ser Tyr Glu Asn Asp  
115 120 125

Ala Phe Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala  
130 135 140

Ser Thr Lys  
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20 25 30

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe  
35 40 45

51791AUSC1.ST25.txt

Ser Ser Tyr Val Met His Trp Leu Arg Gln Ala Pro Gly Lys Gly Leu  
50 55 60

Glu Trp Val Ser Val Ile Gly Thr Gly Gly Val Thr His Tyr Ala Asp  
65 70 75 80

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser  
85 90 95

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr  
100 105 110

Tyr Cys Ala Arg Trp Gly Tyr Tyr Gly Ser Gly Ser Tyr Glu Asn Asp  
115 120 125

Ala Phe Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala  
130 135 140

Ser Thr Lys  
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<213> Homo sapiens

<400> 29

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1 5 10 15

Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser  
20 25 30

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser  
35 40 45

Val Ser Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala  
50 55 60

Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro  
65 70 75 80

Asp Arg Phe Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile  
85 90 95

51791AUSC1.ST25.txt

Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr  
100 105 110

Gly Ser Ser Leu Thr Phe Gly Gly Thr Lys Val Glu Ile Lys  
115 120 125

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Met Glu Phe Val Leu Ser Trp Val Phe Leu Val Ala Ile Leu Lys Gly  
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Val Gln Cys Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Met  
20 25 30

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe  
35 40 45

Ser Ser Tyr Val Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu  
50 55 60

Glu Trp Val Ser Val Ile Gly Thr Gly Gly Val Thr Asn Tyr Ala Asp  
65 70 75 80

Ser Val Lys Gly Arg Phe Met Ile Ser Arg Asp Asn Ala Lys Asn Ser  
85 90 95

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr  
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Tyr Cys Ala Arg Trp Gly Asp Trp Asp Asp Ala Phe Asp Ile Trp Gly  
115 120 125

Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys  
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Met Glu Phe Val Leu Ser Trp Val Phe Leu Val Ala Ile Leu Lys Gly

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Val Gln Cys Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln  
20 25 30

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe  
35 40 45

Ser Ser Tyr Val Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu  
50 55 60

Glu Trp Val Ser Val Ile Gly Thr Gly Gly Val Thr Asn Tyr Ala Asp  
65 70 75 80

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser  
85 90 95

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr  
100 105 110

Tyr Cys Ala Arg Trp Gly Asp Trp Asp Asp Ala Phe Asp Ile Trp Gly  
115 120 125

Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys  
130 135 140